




















Related Structures

Sequences producing significant alignments:	Score (bits)	E Value	
gi 309818 gb AAA33784.1 antigen	32	1.4	
gi 22958582 ref ZP_00006250.1 COG1360: Flagellar motor pro...	29	7.9	
gi 20150316 pdb 1J45 A Chain A, Structure Of Artocarpin: A ...	28	14	
gi 26347287 dbj BAC37292.1 unnamed protein product [Mus mu...	28	14	
gi 34873522 ref XP_220904.2 similar to hypothetical protei...	28	19	
gi 309820 gb AAA33785.1 Antigen	28	19	
gi 16041188 dbj BAB69761.1 hypothetical protein [Macaca fa...	28	19	
gi 34899222 ref NP_910957.1 alcohol dehydrogenase-like pro...	28	19	
gi 31242129 ref XP_321495.1 ENSANGP00000025339 [Anopheles ...	27	26	
gi 499385 emb CAA53511.1 collectin-43 [Bos taurus]	27	26	
gi 21436533 emb CAD29637.1 putative 5-oxoprolinase [Anophe...	27	26	
gi 27923966 sp P42916 CL43_BOVIN Collectin-43 precursor (CL...	27	26	
gi 1083017 pir A53570 collectin-43 - bovine	27	26	
gi 6753710 ref NP_034228.1 opsin (encephalopsin); encephal...	27	34	

gi 22971781 ref ZP_00018707.1 	hypothetical protein [Chloro...	27	34
gi 31982388 ref NP_783630.2 	conglutinin 1 [Bos taurus] >gi...	27	46
gi 10719868 sp Q9QYC0 ADDA MOUSE	Alpha adducin (Erythrocyte...	27	46
gi 27676688 ref XP_218355.1 	similar to hypothetical protei...	27	46
gi 34873860 ref XP_343971.1 	similar to Mox-1 [Rattus norve...	27	46
gi 27711226 ref XP_213841.1 	similar to RIKEN cDNA 1110002H...	27	46
gi 21706416 gb AAH34368.1 	Add1 protein [Mus musculus]	27	46
gi 12844579 dbj BAB26417.1 	unnamed protein product [Mus mu...	27	46
gi 7304861 ref NP_038485.1 	adducin 1 (alpha) [Mus musculus...	27	46
gi 461774 sp P23805 CONG BOVIN	CONGLUTININ PRECURSOR >gi 34...	27	46
gi 8850211 ref NP_058686.1 	adducin 1, alpha [Rattus norveg...	27	46
gi 26988441 ref NP_743866.1 	fumarylacetoacetate hydrolase ...	27	46
gi 29570599 emb CAD69922.1 	surfactant protein D [Bos taurus]	27	46
gi 14579673 gb AAK69357.1 	pericentriolar material 1 protei...	27	46
gi 27923754 sp Q8MHZ9 CL46 BOVIN	Collectin-46 precursor (CL...	27	46
gi 395268 emb CAA50665.1 	conglutinin [Bos taurus]	27	46
gi 6754680 ref NP_034921.1 	mesenchyme homeobox 1 [Mus musc...	27	46
gi 1083589 pir S54147	alpha adducin - rat	27	46
gi 19352357 ref NP_598115.1 	OprJ protein [uncultured bacte...	27	46
gi 18959276 ref NP_036316.1 	forkhead box D4-like 1 [Homo s...	26	62
gi 38081917 ref XP_132038.2 	stromal interaction molecule 2...	26	62
gi 32405518 ref XP_323372.1 	predicted protein [Neurospora ...	26	62
gi 34451549 gb AAQ72339.1 	FOX D4 [Gorilla gorilla]	26	62
gi 39979247 emb CAE85616.1 	hypothetical protein [Neurospor...	26	62
gi 38648940 gb AAH63191.1 	Unknown (protein for MGC:75588) ...	26	62
gi 27378759 ref NP_770288.1 	bll3648 [Bradyrhizobium japoni...	26	83
gi 7516461 pir E72614	hypothetical protein APE1374 - Aerop...	26	83
gi 7025451 gb AAF35887.1 	somatostatin receptor-interacting...	26	83
gi 4850168 gb AAD04569.2 	synaptic SAPAP-interacting protei...	26	83
gi 11968152 ref NP_057232.1 	SH3 and multiple ankyrin repea...	26	83
gi 7519945 pir A58801	mannose-specific lectin KM+ - Artoca...	26	83
gi 4140029 dbj BAA36973.1 	alpha 1 type I collagen [Cynops ...	25	112
gi 27734098 ref NP_775623.1 	Eph receptor B1 [Mus musculus]...	25	112
gi 2739208 gb AAB94627.1 	Eph-like receptor tyrosine kinase...	25	112
gi 26349347 dbj BAC38313.1 	unnamed protein product [Mus mu...	25	112
gi 10442535 gb AAG17360.1 	interphotoreceptor retinoid bind...	25	112
gi 29655054 ref NP_820746.1 	ferrous iron transport protein...	25	112
gi 9625581 ref NP_039832.1 	Hypothetical protein [Human her...	25	112
gi 4758284 ref NP_004432.1 	ephrin receptor EphB1 precursor...	25	112
gi 34870072 ref XP_213685.2 	similar to CG33130-PA [Rattus ...	25	112
gi 38089043 ref XP_133997.4 	RIKEN cDNA 2310057J16 [Mus mus...	25	112
gi 38101266 gb EAA48254.1 	hypothetical protein MG10317.4 [...	25	112
gi 21224968 ref NP_630747.1 	conserved hypothetical protein...	25	112
gi 4104411 gb AAD02030.1 	Eph-like receptor tyrosine kinase...	25	112
gi 34327988 dbj BAB67820.2 	KIAA1927 protein [Homo sapiens]	25	112
gi 29179544 gb AAH48787.1 	Similar to RIKEN cDNA 4930541M15...	25	112
gi 16121180 ref NP_404493.1 	hypothetical protein [Yersinia...	25	112
gi 12328471 dbj BAB21131.1 	P0416D03.19 [Oryza sativa (japo...	25	112
gi 27721289 ref XP_217250.1 	similar to Ephrin type-B recep...	25	112
gi 23613524 ref NP_704545.1 	erythrocyte membrane protein 1...	25	112
gi 29827065 ref NP_821699.1 	hypothetical protein [Streptom...	25	150


gi 38045919 ref NP_005329.3	huntingtin interacting protein...	25	150	
gi 15004817 ref NP_149277.1	Possible beta-xylosidase, fami...	25	150	
gi 20913895 ref XP_147630.1	hypothetical protein XP_147630...	25	150	
gi 2499164 sp Q52992 YNF7_RHIME	HYPOTHETICAL 25.1 KDA PROTE...	25	150	
gi 6678339 ref NP_033404.1	thrombomodulin [Mus musculus] >...	25	150	
gi 28396081 gb AAO39202.1	nuclear receptor NHR-114 [Caenor...	25	150	
gi 2072423 gb AAC51257.1	huntingtin interacting protein 1 ...	25	150	
gi 755724 emb CAA88565.1	alpha-toxin [Clostridium novyi]	25	150	
gi 15234502 ref NP_192399.1	hypothetical protein [Arabidop...	25	150	
gi 27960450 gb AAO27833.1	nuclear receptor protein [Caenor...	25	150	
gi 21234145 ref NP_639722.1	hypothetical protein [Streptom...	25	150	
gi 731074 sp P40349 URB1_USTMA	Siderophore biosynthesis reg...	25	150	
gi 2144160 pir S55805	alpha-toxin - Clostridium novyi (ATC...	25	150	
gi 17565736 ref NP_504164.1	nuclear Hormone Receptor (nhr-...	25	150	
gi 5174543 ref NP_005910.1	MADS box transcription enhancer...	24	201	
gi 30851578 gb AAH52428.1	Coll15a1 protein [Mus musculus]	24	201	
gi 34896876 ref NP_909782.1	hypothetical protein [Oryza sa...	24	201	
gi 6978677 ref NP_037061.1	procollagen, type II, alpha 1; ...	24	201	
gi 23018969 ref ZP_00058682.1	COG0545: FKBP-type peptidyl-...	24	201	
gi 7462033 pir T30910	xylanase (EC 3.2.1.-) - Caldocellum ...	24	201	
gi 34879634 ref XP_214400.2	similar to collagen alpha 1(IV...	24	201	
gi 30842815 ref NP_783186.2	disrupted in schizophrenia 1 [...	24	201	
gi 18313160 ref NP_559827.1	3-hydroxy-3-methylglutaryl-coe...	24	201	
gi 23121576 ref ZP_00103825.1	COG0243: Anaerobic dehydroge...	24	201	
gi 18202034 sp Q42350 CA21_RANCA	Collagen alpha 2(I) chain ...	24	201	
gi 38344719 emb CAE05261.2	OSJNBb0115I09.23 [Oryza sativa ...	24	201	
gi 50502 emb CAA29946.1	unnamed protein product [Mus muscu...	24	201	
gi 15241519 ref NP_199263.1	small nuclear ribonucleoprotei...	24	201	
gi 33859528 ref NP_034061.1	procollagen, type IV, alpha 1 ...	24	201	
gi 18496907 ref NP_569757.1	minor tail subunit gp21 [Mycob...	24	201	
gi 15241657 ref NP_195818.1	zinc finger (C3HC4-type RING f...	24	201	
gi 39997046 ref NP_952997.1	hypothetical protein GSU1948 [...	24	269	
gi 38100524 gb EAA47639.1	predicted protein [Magnaporthe g...	24	269	
gi 24981080 gb AAH39762.1	Unknown (protein for IMAGE:40102...	24	269	
gi 16356979 ref NP_443630.1	ND6 15838 NADH dehydrogenase su...	24	269	

Alignments

Get selected sequences

Select all

Deselect all

 >gi|309818|gb|AAA33784.1| antigen
Length = 386

Score = 31.6 bits (67), Expect = 1.4

Identities = 13/20 (65%); Positives = 13/20 (65%), Gaps = 3/20 (15%)

Query: 3 QGPAGSGWEEGSGSPPGVTP 22
Q P A G S G S G S P P V P
Sbjct: 126 QAPAGSS---GSGSPPAVPP 142

>[gi|22958582|ref|ZP_00006250.1|](#) COG1360: Flagellar motor protein [Rhodobacter sp]
Length = 366

Score = 29.1 bits (61), Expect = 7.9
Identities = 11/16 (68%), Positives = 13/16 (81%), Gaps = 2/16 (12%)

Query: 4 GPAGSGWEEGSGSPPG 19
GPAG G EG+G+PPG
Sbjct: 189 GPAGPG--EGTGAPPG 202

>[gi|20150316|pdb|1J4S|A](#) Chain A, Structure Of Artocarpin: A Lectin With Mannos
Specificity (Form 1)
[gi|20150317|pdb|1J4S|B](#) Chain B, Structure Of Artocarpin: A Lectin With Mannose
Specificity (Form 1)
[gi|20150318|pdb|1J4S|C](#) Chain C, Structure Of Artocarpin: A Lectin With Mannose
Specificity (Form 1)
[gi|20150319|pdb|1J4S|D](#) Chain D, Structure Of Artocarpin: A Lectin With Mannose
Specificity (Form 1)
Length = 149

Score = 28.2 bits (59), Expect = 14
Identities = 8/11 (72%), Positives = 10/11 (90%)

Query: 4 GPAGSGWEEGS 14
GP G+GW+EGS
Sbjct: 12 GPGGNGWDEGS 22

>[gi|26347287|dbj|BAC37292.1|](#) unnamed protein product [Mus musculus]
Length = 280

Score = 28.2 bits (59), Expect = 14
Identities = 16/28 (57%), Positives = 17/28 (60%), Gaps = 9/28 (32%)

Query: 6 AGSGWE-EGSGS-----PPGVTPPLFSP 26
AGSG E EGS + PPG TP FSP
Sbjct: 34 AGSG-EAEGSSASSPSLPPPG-TPAFSP 59

>[gi|34873522|ref|XP_220904.2|](#) similar to hypothetical protein 4932418K24 [Ratt]
Length = 747


Score = 27.8 bits (58), Expect = 19
Identities = 8/11 (72%), Positives = 10/11 (90%)

Query: 16 SPPGVTPPLFSP 26
SPPG +PLF+P
Sbjct: 112 SPPGASPLFTP 122

>[gi|309820|gb|AAA33785.1|](#) Antigen
Length = 417


Score = 27.8 bits (58), Expect = 19
 Identities = 11/16 (68%), Positives = 11/16 (68%), Gaps = 3/16 (18%)

Query: 3 QGPAGSGWEEGSGSPP 18
 Q PAGS GSGSPP
 Sbjct: 160 QAPAGSS---GSGSPP 172

 >[gi|16041188|dbj|BAB69761.1|](#) hypothetical protein [Macaca fascicularis]
 Length = 135


Score = 27.8 bits (58), Expect = 19
 Identities = 14/28 (50%), Positives = 14/28 (50%), Gaps = 9/28 (32%)

Query: 4 GPAG-SGWEEGSGSP-----PGVTP 22
 GP G SGWE G SP P VTP
 Sbjct: 83 GPVGASGWEAGCASPQPTSLTPYPRVTP 110

 >[gi|34899222|ref|NP_910957.1|](#) alcohol dehydrogenase-like protein~contains EST C7
 [Oryza sativa (japonica cultivar-group)]
 Length = 462



Score = 27.8 bits (58), Expect = 19
 Identities = 12/19 (63%), Positives = 12/19 (63%), Gaps = 2/19 (10%)

Query: 5 PAGSGWEEGSGSPPGVTP 23
 PAGSG E GSPP V L
 Sbjct: 405 PAGSGRGE--GSPPAVKSL 421

 >[gi|31242129|ref|XP_321495.1|](#) ENSANGP00000025339 [Anopheles gambiae]
[gi|19572990|emb|CAD28130.1|](#) putative 5-oxoprolinase [Anopheles gambiae]
[gi|30173744|gb|EAA43140.1|](#) ENSANGP00000025339 [Anopheles gambiae str. PEST]
 Length = 1344


Score = 27.4 bits (57), Expect = 26
 Identities = 11/15 (73%), Positives = 12/15 (80%), Gaps = 3/15 (20%)

Query: 11 EEGSG-SPPG--VTP 22
 EEGSG +PPG VTP
 Sbjct: 688 EEGSGQAPPGRVTP 702

 >[gi|499385|emb|CAA53511.1|](#)  collectin-43 [Bos taurus]
 Length = 301



Score = 27.4 bits (57), Expect = 26
 Identities = 15/26 (57%), Positives = 16/26 (61%), Gaps = 6/26 (23%)

Query: 1 GMQGPAG----SGWEEGSGSPPGVTP 22
 GM GPAG SG +GS PPG TP
 Sbjct: 50 GMPGPAGREGPSGR-QGSMGPPG-TP 73

 >[gi|21436533|emb|CAD29637.1|](#) putative 5-oxoprolinase [Anopheles gambiae]
Length = 756


Score = 27.4 bits (57), Expect = 26
Identities = 11/15 (73%), Positives = 12/15 (80%), Gaps = 3/15 (20%)

Query: 11 EEGSG-SPPG--VTP 22
EEGSG +PPG VTP
Sbjct: 644 EEGSGQAPPGRVTP 658

 >[gi|27923966|sp|P42916|CL43 BOVIN](#) Collectin-43 precursor (CL-43) (43 kDa collect
[gi|18252109|gb|AAL61855.1|](#)  43kDa collectin precursor [Bos taurus]
[gi|18252111|gb|AAL61856.1|](#) 43kDa collectin precursor [Bos taurus]
Length = 321





Score = 27.4 bits (57), Expect = 26
Identities = 15/26 (57%), Positives = 16/26 (61%), Gaps = 6/26 (23%)

Query: 1 GMQGPAG----SGWEEGSGSPPGVTP 22
GM GPAG SG +GS PPG TP
Sbjct: 70 GMPGPAGREGPSGR-QGSMGPPG-TP 93

 >[gi|1083017|pir||A53570](#) collectin-43 - bovine
Length = 301


Score = 27.4 bits (57), Expect = 26
Identities = 15/26 (57%), Positives = 16/26 (61%), Gaps = 6/26 (23%)

Query: 1 GMQGPAG----SGWEEGSGSPPGVTP 22
GM GPAG SG +GS PPG TP
Sbjct: 50 GMPGPAGREGPSGR-QGSMGPPG-TP 73

 >[gi|6753710|ref|NP_034228.1|](#)  opsin (encephalopsin); encephalopsin [Mus musculu
[gi|18203573|sp|Q9WUK7|OPN3 MOUSE](#) Opsin 3 (Encephalopsin) (Panopsin)
[gi|4894950|gb|AAD32670.1|](#)  encephalopsin [Mus musculus]
[gi|26335541|dbj|BAC31471.1|](#)  unnamed protein product [Mus musculus]
[gi|27463274|gb|AAO15719.1|](#) encephalopsin [Mus musculus]
Length = 400

Score = 26.9 bits (56), Expect = 34
Identities = 11/24 (45%), Positives = 14/24 (58%), Gaps = 7/24 (29%)

Query: 10 WEEGSGS----PPGV---TPLFSP 26
WE+G+G+ P G PLFSP
Sbjct: 13 WEDGAGAEAGAAPAGTRSPAPLFSP 36

 >[gi|22971781|ref|ZP_00018707.1|](#) hypothetical protein [Chloroflexus aurantiacus]